

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 10:18:03 ; Search time 17609 Seconds
 (without alignments)
 . 11497.390 Million cell updates/sec

Title: US-10-501-930-2

Perfect score: 3166

Sequence: 1 cgagcggcgagtcggtgcc.....gctattagcaaaaaaaaaaa 3166

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*

1: gb_env:*

2: gb_pat:*

3: gb_ph:*

4: gb_pl:*

5: gb_pr:*

6: gb_ro:*

7: gb_sts:*

8: gb_sy:*

9: gb_un:*

10: gb_vi:*

11: gb_ov:*

12: gb_htg:*

13: gb_in:*

14: gb_om:*

15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	3166	100.0	3166	6	AB059554	AB059554 Mus muscu
c	2361	74.6	110000	12	BX322642_0	BX322642 Mus muscu
3	2361	74.6	110000	12	BX322642_2	Continuation (3 of
c	2361	74.6	110000	12	BX322642_2	Continuation (3 of
c	2361	74.6	202001	6	AL772303	AL772303 Mouse DNA
6	1408.4	44.5	236283	12	AC120773	AC120773 Rattus no
c	1408.4	44.5	264245	12	AC096804	AC096804 Rattus no

8	1028	32.5	1197	6	AJ699423	AJ699423 Rattus no	
9	861.8	27.2	1234	5	AJ621583	AJ621583 Homo sapi	
10	857.8	27.1	1197	5	AJ697663	AJ697663 Pan trogl	
11	757	23.9	1197	14	AJ868431	AJ868431 Bos tauru	
12	559.8	17.7	1149	2	CQ736679	CQ736679 Sequence	
c	13	470.4	14.9	151289	5	AL158164	AL158164 Human DNA
14	467.2	14.8	1197	11	AJ699424	AJ699424 Gallus ga	
15	456.8	14.4	1520	11	CR352448	CR352448 Gallus ga	
16	381	12.0	112099	12	AC143457	AC143457 Macaca mu	
17	257.8	8.1	493	7	BV211170	BV211170 SIAT8F _5	
18	256.6	8.1	1334	11	AJ704564	AJ704564 Gallus ga	
19	248.2	7.8	1140	11	AJ715548	AJ715548 Tetraodon	
20	247.6	7.8	1131	6	AJ699422	AJ699422 Rattus no	
21	244	7.7	1131	5	AJ697662	AJ697662 Pan trogl	
22	244	7.7	1131	5	CR457037	CR457037 Homo sapi	
23	244	7.7	1878	2	CQ721379	CQ721379 Sequence	
24	244	7.7	1953	5	BC108910	BC108910 Homo sapi	
25	244	7.7	1953	5	BC108911	BC108911 Homo sapi	
26	242.8	7.7	1881	6	BC034855	BC034855 Mus muscu	
27	242.4	7.7	2594	5	AK056270	AK056270 Homo sapi	
28	241.2	7.6	1854	6	MMA28ST	X98014 M.musculus	
29	239.2	7.6	1899	5	HSU91641	U91641 Human alpha	
30	237.8	7.5	2135	5	AK094273	AK094273 Homo sapi	
31	234.4	7.4	1125	14	AJ868432	AJ868432 Bos tauru	
32	231.6	7.3	2094	5	AK130126	AK130126 Homo sapi	
33	228.8	7.2	1032	11	AJ715546	AJ715546 Danio rer	
34	228.2	7.2	1137	11	AJ871609	AJ871609 Oryzias l	
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36	224.4	7.1	1630	5	HUMGD3G	L43494 Human gangl	
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38	224.4	7.1	1755	2	CQ721891	CQ721891 Sequence	
39	224.4	7.1	2117	2	AR360634	AR360634 Sequence	
40	224.4	7.1	2117	5	HSGD3S	X77922 H.sapiens G	
41	222.8	7.0	1650	5	HUM28SIATR	L32867 Homo sapien	
42	221.2	7.0	1071	5	AJ697658	AJ697658 Pan trogl	
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44	220.4	7.0	1140	11	AJ715547	AJ715547 Takifugu	
45	211.6	6.7	2381	6	BC024821	BC024821 Mus muscu	

ALIGNMENTS

RESULT 1

AB059554

LOCUS AB059554 3166 bp mRNA linear ROD 27-APR-2005
 DEFINITION Mus musculus ST8Sia VI mRNA for alpha 2,8-sialyltransferase, complete cds.
 ACCESSION AB059554
 VERSION AB059554.1 GI:21668466
 KEYWORDS .
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Takashima,S., Ishida,H.K., Inazu,T., Ando,T., Ishida,H., Kiso,M., Tsuji,S. and Tsujimoto,M.
 TITLE Molecular cloning and expression of a sixth type of alpha 2,8-sialyltransferase (ST8Sia VI) that sialylates O-glycans

JOURNAL J. Biol. Chem. 277 (27), 24030-24038 (2002)
 PUBMED 11980897
 REFERENCE 2 (bases 1 to 3166)
 AUTHORS Takashima, S.
 TITLE Direct Submission
 JOURNAL Submitted (07-APR-2001) Shou Takashima, RIKEN, Cellular
 Biochemistry Laboratory; 2-1 Hirosawa, Wako, Saitama, 351-0198,
 Japan (E-mail:staka@riken.jp, Tel:81-48-462-1111(ex.3424),
 Fax:81-48-462-4670)
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 /mol_type="mRNA"
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 /country="Japan"
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 CDS 77. .1273
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 PVGTNMSYEVESKK
 HIPIRENIFHMFPVSPQFVDYPYNQCAVVGNGGILNKSCLGAEIDKSDFVRCNLPP
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ORIGIN

Query Match 100.0%; Score 3166; DB 6; Length 3166;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CGGAGCGCGAGTCGGTGCCGCCGGCTGCGCTTCGCCCGGCAGCTTGGCGGCAGG 60
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 Db 1 CGGAGCGCGAGTCGGTGCCGCCGGCTGCGCTTCGCCCGGCAGCTTGGCGGCAGG 60

 Qy 61 ACGCCCGTGGCTCAGGATGAGATCGGGGGCACGCTGTTGCCCTCATAGGCAGCCTGAT 120
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 Qy 121 GCTGCTGCTCCTCGTATGCTCTGGTGCCCAGCCAGCGCCCTGCCGCTCCAGGCT 180
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 Db 121 GCTGCTGCTCCTCGTATGCTCTGGTGCCCAGCCAGCGCCCTGCCGCTCCAGGCT 180

 Qy 181 GTTGATGGAGGAAGCAGAGAGGACACCAGTGGTACCTCAGCTGCACTGAAGACACTCTG 240
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 Qy 241 GAGCCCGACAACCCCGTACCAACGCACCAAGGAACAGCACATATCTGGATGAGAACAAAC 300
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Qy	481	CATTCAAGACTTCGTGGTTCCCAGAACAAACACTCCAGTGGGACTAACATGAGCTACGA	540
Db	481	CATTCAAGACTTCGTGGTTCCCAGAACAAACACTCCAGTGGGACTAACATGAGCTACGA	540
Qy	541	GGTGGAAAGCAAGAACACATCCCCATTGAGAGAACATTCCACATGTTCCAGTGTGTC	600
Db	541	GGTGGAAAGCAAGAACACATCCCCATTGAGAGAACATTCCACATGTTCCAGTGTGTC	600
Qy	601	GCAGCCTTTGTGGACTATCCCTATAACCAGTGTGCAGTGGTTGTAATGGGGAATTCT	660
Db	601	GCAGCCTTTGTGGACTATCCCTATAACCAGTGTGCAGTGGTTGTAATGGGGAATTCT	660
Qy	661	CAACAAGTCTCTCGGGAGCAGAAATTGATAAAATCTGACTTCGTCTCAGGTGTAACT	720
Db	661	CAACAAGTCTCTCGGGAGCAGAAATTGATAAAATCTGACTTCGTCTCAGGTGTAACT	720
Qy	721	CCCCCAATCACAGGGAGCGCTAGTAAAGATGTTGAAGCAAAACAAATCTTGTGACTGT	780
Db	721	CCCCCAATCACAGGGAGCGCTAGTAAAGATGTTGAAGCAAAACAAATCTTGTGACTGT	780
Qy	781	CAATCCCAGCATTATAACCCTGAAGTACCAAGAATTGAAGGAGAAGAACAGTTTT	840
Db	781	CAATCCCAGCATTATAACCCTGAAGTACCAAGAATTGAAGGAGAAGAACAGTTTT	840
Qy	841	GGAGGACATCTCACCTATGGAGATGCATTCCCTCCTGCCAGCATTTCTATCGGGC	900
Db	841	GGAGGACATCTCACCTATGGAGATGCATTCCCTCCTGCCAGCATTTCTATCGGGC	900
Qy	901	CAACACAGGCATCTTTAAAGTCTACCAACACTCAAAGAGTCAAAATGAGGCAAA	960
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Qy	1021	GGTGAACATACCGTTGTCCACAGGCTTGTGATGATTGCAAGTGTGCTGTGAACTGTG	1080
Db	1021	GGTGAACATACCGTTGTCCACAGGCTTGTGATGATTGCAAGTGTGCTGTGAACTGTG	1080
Qy	1081	TGAAACAGCTACGGATTCTGGCCTTCTAAGACTATCGAAGACACCCCACT	1140
Db	1081	TGAAACAGCTACGGATTCTGGCCTTCTAAGACTATCGAAGACACCCCACT	1140
Qy	1141	CAGTCACCAACTATGATAACATGTTACCTAACGATGGTTCCACCAGATGCCTAAAGA	1200
Db	1141	CAGTCACCAACTATGATAACATGTTACCTAACGATGGTTCCACCAGATGCCTAAAGA	1200
Qy	1201	ATACAGCCAATGCTCCAGCTCCATATGAGAGGAATCCTCAAACGTCAATTGCAATG	1260
Db	1201	ATACAGCCAATGCTCCAGCTCCATATGAGAGGAATCCTCAAACGTCAATTGCAATG	1260
Qy	1261	TGAAACGGCTAACGTTCTAGAAGGAGATAATTCAAGGAGGTGGAGTGGATGTGTCA	1320

Db	1261	TGAAACGGCTAACGTTCTAGAAGGAGAATAATTCAAGGAGGTGGAGTGGATGTCA	1320
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Db	1321	CAGCATCTCCAAAAGCCAATAGAAGAAGGCACAGAGAAAGCATGAATTACAAAGGCCT	1380
Qy	1381	CTCCCACTTGTCTAGACCAAAGCCACCCGCCCTCACTTTGCAGCCTCACGAGTCA	1440
Db	1381	CTCCCACTTGTCTAGACCAAAGCCACCCGCCCTCACTTTGCAGCCTCACGAGTCA	1440
Qy	1441	CTCATTCTCACCTCAACGTTCTCTGAGAATAGAGACCAAAACATCAGACTGGAT	1500
Db	1441	CTCATTCTCACCTCAACGTTCTCTGAGAATAGAGACCAAAACATCAGACTGGAT	1500
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Db	1561	GAATGCTCCTGTTCTATCCATGATAGCCATTCCACCTTATCAGAGTGGTAATGAA	1620
Qy	1621	ACTGTGCAATTGTGCCAAGACCCTTCTGAAGAGAATGTCTGAATCATGCGCCGAGTT	1680
Db	1621	ACTGTGCAATTGTGCCAAGACCCTTCTGAAGAGAATGTCTGAATCATGCGCCGAGTT	1680
Qy	1681	TTACACACAGCTTCCTTATAAAATCCTCCATTCTCCCTCTAGTAGAGTACA	1740
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Qy	1741	GAAACAAAATACCCATTGATGATTCAAGGAAGAAAAGTCTTTTACTTAGCAATGTGCCTG	1800
Db	1741	GAAACAAAATACCCATTGATGATTCAAGGAAGAAAAGTCTTTTACTTAGCAATGTGCCTG	1800
Qy	1801	CTTCTGATTCAAGTCGTTGTGACATTAAGCTGGGTGGGTTGGTGGATTTGGGC	1860
Db	1801	CTTCTGATTCAAGTCGTTGTGACATTAAGCTGGGTGGGTTGGTGGATTTGGGC	1860
Qy	1861	GTTTCTTCACTTCTTTGTCTATATTCCTACCTTATCAGTTGTATTGAGCTTCC	1920
Db	1861	GTTTCTTCACTTCTTTGTCTATATTCCTACCTTATCAGTTGTATTGAGCTTCC	1920
Qy	1921	TGCTTTGGGATTCTGCAATTCTCTCCCCTGACAGGATCAACTCAATGACATAAAGTA	1980
Db	1921	TGCTTTGGGATTCTGCAATTCTCTCCCCTGACAGGATCAACTCAATGACATAAAGTA	1980
Qy	1981	GTTCAACATCCATTGTTCTCACATGTTATCCATAAAGTTACTCATCTGATTATT	2040
Db	1981	GTTCAACATCCATTGTTCTCACATGTTATCCATAAAGTTACTCATCTGATTATT	2040
Qy	2041	TAAAATAGTGAACATCTACTTGTATCAGACCCGAGGACCATCCTCATTGGAGAATATG	2100
Db	2041	TAAAATAGTGAACATCTACTTGTATCAGACCCGAGGACCATCCTCATTGGAGAATATG	2100
Qy	2101	AAGATATTGTCACTGGCAGAAAAGCAGGTGTGCCATTGATAAGATACCACAAGC	2160
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Qy	2401 TGTGAGGCTACGCTAAAACCTCTGCGTAGGGAGAGAGTACAGTCATGAGTGTGGCGGCT	2460
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Qy	2461 TTTGTCCACACTCGTGAAGGGTGAGTAATTCAAGGCCAATCACATCACAGGATGGACAC	2520
Db	2461 TTTGTCCACACTCGTGAAGGGTGAGTAATTCAAGGCCAATCACATCACAGGATGGACAC	2520
Qy	2521 ACCTAACTCATCACTCAGGGGGAGATGAATGCTTCATGAGAAATTACACTCATAAGCT	2580
Db	2521 ACCTAACTCATCACTCAGGGGGAGATGAATGCTTCATGAGAAATTACACTCATAAGCT	2580
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Qy	2701 AAATGCTTATGTCGTATATTCTGTTCATCCATCGATTTCACAGGAAAGTAAGAGCATAG	2760
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Qy	2761 GAGATGAGGCCTACATGCCAAGAAAACATATAAATTACTCTTAATTCTTACTTGAGCC	2820
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Db	2821 AGCTTGTGTTATCAAGTGCTTTTGAAAGAGACAGCACCCCTGTGAATTCTTCATTCTG	2880
Qy	2881 ATACAGTGTACCTTGATTTAACATTGTAATGTTGTTCAAGTTACATCTCTTCAT	2940
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Qy	3001 ATTTTGCAAAGGGTAAAGGCTTTTGTAAATAAAATAAAATTATTATTCTCTG	3060
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Qy	3061 ATGAATAGAGGCTTTTATGCTGCTGCTAATGAACCTAATTAGCTTAAATTATCTCCT	3120
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Qy 3121 AGAACATTGGTCACGTTCAATCATGCTATTAGCAAAAAAAA 3166
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SCORE Search Results Details for Application 10501930 and Search Result us-10-501-930-1.rup.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10501930 and Search Result us-10-501-930-1.rup.

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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:22:24 ; Search time 302 Seconds
(without alignments)
1219.060 Million cell updates/sec

Title: US-10-501-930-1

Perfect score: 2102

Sequence: 1 MRSGGTLFALIGSLMLLLL.....MLQLHMRGILKLOFSKCETA 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Query Score	Match	Length	DB	ID	Description
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1	2102	100.0	398	1	SIA8F_MOUSE	Q8k4t1 mus musculu
2	2102	100.0	405	2	Q3T9N4_MOUSE	Q3t9n4 mus musculu
3	1936	92.1	398	2	Q6ZXC7_RAT	Q6zxc7 rattus norv
4	1922	91.4	362	2	Q8BI43_MOUSE	Q8bi43 mus musculu

5	1772	84.3	398	1	SIA8F_HUMAN	P61647 homo sapien
6	1772	84.3	398	2	Q5VZH4_HUMAN	Q5vzh4 homo sapien
7	1763	83.9	398	1	SIA8F_PANTR	P61648 pan troglod
8	1597	76.0	398	2	Q5NDG0_BOVIN	Q5ndg0 bos taurus
9	1183	56.3	398	2	Q6ZXC6_CHICK	Q6zxc6 gallus gall
10	728	34.6	343	2	Q6KC02_BRARE	Q6kc02 brachydanio
11	727.5	34.6	379	2	Q6KC00_TETNG	Q6kc00 tetraodon n
12	725.5	34.5	378	2	Q5K019_ORYLA	Q5k019 oryzae lat
13	719.5	34.2	372	2	Q50J40_FUGRU	Q50j40 fugu rubrip
14	719.5	34.2	379	2	Q6KC01_FUGRU	Q6kc01 fugu rubrip
15	715.5	34.0	356	2	Q6KBZ7_BRARE	Q6kbz7 brachydanio
16	710.5	33.8	342	2	P79783_CHICK	P79783 gallus gall
17	703	33.4	356	1	SIA8A_PANTR	P61642 pan troglod
18	702	33.4	342	2	Q78EI9_9MURI	Q78ei9 rattus sp.
19	701	33.3	356	2	P70554_RAT	P70554 rattus norv
20	700	33.3	356	1	SIA8A_HUMAN	Q92185 homo sapien
21	700	33.3	356	2	Q6ZXD2_BOVIN	Q6zxd2 bos taurus
22	700	33.3	412	1	SIA8E_MOUSE	P70126 mus musculu
23	699.5	33.3	370	2	Q6KBZ8_FUGRU	Q6kbz8 fugu rubrip
24	697	33.2	355	2	Q8BL76_MOUSE	Q8bl76 mus musculu
25	697	33.2	355	2	Q8K1C1_MOUSE	Q8k1c1 mus musculu
26	692	32.9	376	2	Q3TRR3_MOUSE	Q3trr3 mus musculu
27	691	32.9	355	2	Q8BWI0_MOUSE	Q8bwi0 mus musculu
28	689	32.8	341	2	Q64468_MOUSE	Q64468 mus musculu
29	688	32.7	376	2	Q8JZQ3_MOUSE	Q8jzq3 mus musculu
30	687.5	32.7	359	2	Q6ZXA0_XENLA	Q6zxa0 xenopus lae
31	686	32.6	374	2	Q5NDF9_BOVIN	Q5ndf9 bos taurus
32	686	32.6	376	1	SIA8E_PANTR	P61646 pan troglod
33	686	32.6	376	2	Q6IAW7_HUMAN	Q6iaw7 homo sapien
34	686	32.6	376	2	Q6ZXC8_RAT	Q6zxc8 rattus norv
35	685	32.6	419	2	Q4SUV1_TETNG	Q4suv1 tetraodon n
36	682.5	32.5	338	2	Q6WRU1_XENLA	Q6wrul xenopus lae
37	682	32.4	355	1	SIA8A_MOUSE	Q64687 mus musculu
38	678	32.3	376	2	Q6ZX98_CHICK	Q6zx98 gallus gall
39	677.5	32.2	345	2	Q6DNG6_XENTR	Q6dng6 xenopus tro
40	677	32.2	376	1	SIA8E_HUMAN	O15466 homo sapien
41	674.5	32.1	275	2	Q3V3B1_MOUSE	Q3v3b1 mus musculu
42	670	31.9	369	2	Q6KBZ9_FUGRU	Q6kbz9 fugu rubrip
43	665.5	31.7	268	2	Q50J35_BRARE	Q50j35 brachydanio
44	665.5	31.7	298	2	Q4T001_TETNG	Q4t001 tetraodon n
45	654.5	31.1	335	2	Q6KC12_TETNG	Q6kc12 tetraodon n

ALIGNMENTS

RESULT 1

SIA8F_MOUSE

ID SIA8F_MOUSE STANDARD; PRT; 398 AA.
 AC Q8K4T1;
 DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Alpha-2,8-sialyltransferase 8F (EC 2.4.99.-) (ST8Sia VI).
 GN Name=St8sia6; Synonyms=Siat8f;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA], AND CHARACTERIZATION.
 RX MEDLINE=22086185; PubMed=11980897; DOI=10.1074/jbc.M112367200;
 RA Takashima S., Ishida H.K., Inazu T., Ando T., Ishida H., Kiso M.,
 RA Tsuji S., Tsujimoto M.;
 RT "Molecular cloning and expression of a sixth type of alpha 2,8-
 RT sialyltransferase (ST8Sia VI) that sialylates O-glycans.";
 RL J. Biol. Chem. 277:24030-24038(2002).
 CC -!- FUNCTION: Prefers O-glycans to N-glycans or glycolipids as
 CC acceptor substrates. The minimal acceptor substrate is the NeuAc-
 CC alpha-2,3(6)-Gal sequence at the nonreducing end of their
 CC carbohydrate groups.
 CC -!- PATHWAY: Glycosylation.
 CC -!- SUBCELLULAR LOCATION: Golgi apparatus; Golgi membrane; single-pass
 CC type II membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the glycosyltransferase 29 family.
 CC -----
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 CC -----
 DR EMBL; AB059554; BAC01265.1; -; mRNA.
 DR Ensembl; ENSMUSG00000003418; Mus musculus.
 DR MGI; MGI:2386797; st8sia6.
 DR GO; GO:0008373; F:sialyltransferase activity; IDA.
 DR GO; GO:0016051; P:carbohydrate biosynthesis; IDA.
 DR GO; GO:0009247; P:glycolipid biosynthesis; IDA.
 DR GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.
 DR InterPro; IPR001675; Glyco_trans_29.
 DR InterPro; IPR012163; Sialyl_trans.
 DR Pfam; PF00777; Glyco_transf_29; 1.
 DR PIRSF; PIRSF005557; Sialyl_trans; 1.
 KW Glycoprotein; Glycosyltransferase; Golgi stack; Membrane;
 KW Signal-anchor; Transferase; Transmembrane.
 FT CHAIN 1 398 Alpha-2,8-sialyltransferase 8F.
 FT /FTId=PRO_0000149300.
 FT TOPO_DOM 1 3 Cytoplasmic (Potential).
 FT TRANSMEM 4 24 Signal-anchor for type II membrane
 FT protein (Potential).
 FT TOPO_DOM 25 398 Lumenal (Potential).
 FT CARBOHYD 66 66 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 196 196 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 186 335 By similarity.
 SQ SEQUENCE 398 AA; 45428 MW; A73A7A29640D4917 CRC64;

Query Match 100.0%; Score 2102; DB 1; Length 398;
 Best Local Similarity 100.0%; Pred. No. 2.5e-156;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSGGTLFALIGSILMLLLLRMLWCPADAPARSRLLMEGSREDTSGTSAALKTLWSPTTP 60
 |||||||
 Db 1 MRSGGTLFALIGSILMLLLLRMLWCPADAPARSRLLMEGSREDTSGTSAALKTLWSPTTP 60
 |||||||
 Qy 61 VPRTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNQAE 120
 |||||||
 Db 61 VPRTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNQAE 120
 |||||||
 Qy 121 EYDNFRAKLASCCDAIQDFVVSVQNNTPVGTNMSYEVESKKHIPIRENIFHMFVSPQFVD 180
 |||||||
 Db 121 EYDNFRAKLASCCDAIQDFVVSVQNNTPVGTNMSYEVESKKHIPIRENIFHMFVSPQFVD 180

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Qy      181 YPYNQCAVVGNGGILNKSICGAEIDKSDFVFRCLPPIGSASKDVGSKTNLVTVNPSII 240
       ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      181 YPYNQCAVVGNGGILNKSICGAEIDKSDFVFRCLPPIGSASKDVGSKTNLVTVNPSII 240

Qy      241 TLKYQNLKEKKAQFLEDISTYGDAFLLPAFSYRANTGISFKVYQTLKESKMRQKVLFH 300
       ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      241 TLKYQNLKEKKAQFLEDISTYGDAFLLPAFSYRANTGISFKVYQTLKESKMRQKVLFH 300

Qy      301 PRYLRHLALFWRTKGVTAYRLSTGLMIASAVELCENVKLYGFWPFSKTIEDTPLSHYY 360
       ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      301 PRYLRHLALFWRTKGVTAYRLSTGLMIASAVELCENVKLYGFWPFSKTIEDTPLSHYY 360

Qy      361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398
       ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398

```

RESULT 2

Q3T9N4_MOUSE

ID Q3T9N4_MOUSE PRELIMINARY; PRT; 405 AA.

AC Q3T9N4;

DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.

DT 11-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Activated spleen cDNA, RIKEN full-length enriched library,

DE clone:F830206C17 product:sialyltransferase 8 (alpha-2, 8-

DE sialyltransferase) F, full insert sequence.

GN Name=st8sia6;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Activated spleen;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Methods Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Activated spleen;

RX PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,

RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,

RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,

RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,

RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,

RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,

RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,

RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Kitano H., Kollrias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabavsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of"

RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AK172400; BAE42986.1; -; mRNA.
 DR MGI; MGI:2386797; st8sia6.
 DR GO; GO:0008373; F:sialyltransferase activity; IDA.
 DR GO; GO:0016051; P:carbohydrate biosynthesis; IDA.
 DR GO; GO:0009247; P:glycolipid biosynthesis; IDA.
 DR GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.
 DR InterPro; IPR001675; Glyco_trans_29.
 DR InterPro; IPR012163; Sialyl_trans.
 DR Pfam; PF00777; Glyco_transf_29; 1.
 DR PIRSF; PIRSF005557; Sialyl_trans; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 405 AA; 46323 MW; 48B7A17BE3443487 CRC64;

 Query Match 100.0%; Score 2102; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 2.5e-156;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MRSGGTFLALIGSLMLLLLRMLWCPADAPARSRLLMEGSREDTSGTAAALKTLWSPTTP 60
 |||||||
 Db 1 MRSGGTFLALIGSLMLLLLRMLWCPADAPARSRLLMEGSREDTSGTAAALKTLWSPTTP 60
 |||||||
 Qy 61 VPRTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNRQAE 120
 |||||||
 Db 61 VPRTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNRQAE 120
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 Qy 121 EYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMSYEVESKKHPIRENIFHMFVPSQFVD 180
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 Db 121 EYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMSYEVESKKHPIRENIFHMFVPSQFVD 180
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 Qy 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFVFCRNLLPITGSASKDVGSKTNLTVNPSII 240
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 Db 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFVFCRNLLPITGSASKDVGSKTNLTVNPSII 240
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 Qy 241 TLKYQNLKEKKAQFLEDISTYGDAFLLPAFSYRANTGISFKVYQTLKESKMRQKVLFH 300
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 Db 241 TLKYQNLKEKKAQFLEDISTYGDAFLLPAFSYRANTGISFKVYQTLKESKMRQKVLFH 300
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 Qy 301 PRYLRHLALFWRTKGVTAYRLSTGLMIASAVELCENVKLYGFWPFSKTIEDTPLSHYY 360
 |||||||
 Db 301 PRYLRHLALFWRTKGVTAYRLSTGLMIASAVELCENVKLYGFWPFSKTIEDTPLSHYY 360
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 Qy 361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398
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 Db 361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398

RESULT 3

Q6ZXC7_RAT

ID Q6ZXC7_RAT PRELIMINARY; PRT; 398 AA.
 AC Q6ZXC7;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Alpha-2,8-sialyltransferase.
 GN Name=SIAT8F;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Rattus.